

Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
145				150					155				160			
aaa	gtc	ttg	aaa	aca	acc	cag	tct	ggc	ttt	gaa	gga	ttc	atc	aag	gac	528
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
				165					170				175			
cag	ttc	acc	acc	ctc	cct	gag	gtg	aag	gac	cg	tg	ttt	gcc	acc	caa	576
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
				180				185				190				
gtg	tac	tgc	aaa	tgg	cgc	tac	cac	cag	ggc	aga	gat	gtg	gac	ttt	gag	624
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
				195				200				205				
gcc	acc	tgg	gac	act	gtt	agg	agc	att	gtc	ctg	cag	aaa	ttt	gct	ggg	672
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
				210		215			220							
ccc	tat	gac	aaa	ggc	gag	tac	tca	ccc	tct	gtg	cag	aag	acc	ctc	tat	720
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
				225		230			235				240			
gat	atc	cag	gtg	ctc	tcc	ctg	agc	cga	gtt	cct	gag	ata	gaa	gat	atg	768
Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	
				245				250				255				
gaa	atc	agc	ctg	cca	aac	att	cac	tac	ttc	aat	ata	gac	atg	tcc	aaa	816
Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	
				260				265				270				
atg	ggt	ctg	atc	aac	aag	gaa	gag	gtc	ttg	ctg	cca	tta	gac	aat	cca	864
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
				275				280				285				
tat	gga	aaa	att	act	ggt	aca	gtc	aag	agg	aag	ttg	tct	tca	aga	ctg	912
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
				290			295				300					
tga															915	

<210> 2
<211> 304
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PBC CHIMERA

<400> 2
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
65 70 75 80

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln			
35	40	45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat			192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp			
50	55	60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag			240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys			
65	70	75	80
ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag			288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu			
85	90	95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg			336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val			
100	105	110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc			384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val			
115	120	125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa			432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu			
130	135	140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta			480
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu			
145	150	155	160
aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac			528
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp			
165	170	175	
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa			576
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln			
180	185	190	
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag			624
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu			
195	200	205	
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg			672
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly			
210	215	220	
ccc tat gac aaa ggc gag tac tcg ccc tct gtc cag aag aca ctc tat			720
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr			
225	230	235	240
gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg			768
Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met			
245	250	255	
gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa			816
Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys			
260	265	270	
atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca			864
Met Gly Leu Ile Asn Lys Glu Val Leu Leu Pro Leu Asp Asn Pro			
275	280	285	
tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg			912
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu			
290	295	300	

<210> 4
<211> 304
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pks chimera

<400> 4
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro

275

280

285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295 300

<210> 5

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:baboon D3H

<400> 5

Met Ala His Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295 300

<210> 6
<211> 304
<212> PRT
<213> baboon

<400> 6
Met Ala Asp Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295 300

<210> 7
<211> 304
<212> PRT
<213> pig

<400> 7

Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys

260

265

270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285

Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu
 290 295 300

<210> 8
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PBC amino truncated

<400> 8

Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly
 1 5 10 15

Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
 20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220

Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser
 225 230 235 240

Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn
245 250 255

Ile His Tyr Phe Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys
260 265 270

Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly
275 280 285

Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295

<210> 9
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PBC carboxy truncated

<400> 9
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser
290 295 300

<210> 10
<211> 298
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PKS amino truncated

<400> 10
Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly
1 5 10 15

Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
130 135 140

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
210 215 220

Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr
225 230 235 240

Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn
245 250 255

Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys
260 265 270

Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly
275 280 285

Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
290 295

<210> 11
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PKS carboxy truncated

<400> 11
Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser
290 295 300

<210> 12

<211> 915

<212> DNA

<213> PIG

<400> 12

atggctcatt accgtaatga ctacaaaaag aatgatgagg tagagttgt ccgaactggc 60
tatgggaagg atatgataaa agttctccat attcagcgag atggaaaata tcacagcatt 120
aaagaggtgg caacttcagt gcaactgact ttgagctcca aaaaagatta cctgcattgga 180
gacaatttcag atgtcatccc tacagacacc atcaagaaca cagttaatgt cctggcgaag 240
ttcaaggc tcaaaaagcat agaaaacttt gctgtgacta tctgtgagca tttccttct 300
tccttcaggc atgtcatcag agctcaagtc tatgtgaaag aagttccttg gaagcgtttt 360
gaaaagaatg gagttaaagca tgtccatgca tttatttata ctcctactgg aacgcacttc 420
tgtgagggtt aacagataag gaatggacct ccagtcattt attctggaaat caaagaccta 480
aaagtcttga aaacaaccca gtctggcttt gaaggattca tcaaggacca gttcaccacc 540
ctccctgagg tgaaggaccc gtgccttgcc acccaagtgt actgcaaattt gcgctaccac 600
cagggcagag atgtggactt tgagccacc tgggacactg ttaggagcat tgtccctgcag 660
aaatttgctg ggccctatga caaaggcgag tactcgccct ctgtccagaa gacactctat 720
gacatccagg tgctcacccctt gggccagggtt cctgagatag aagatatggaa aatcagcctg 780
ccaaatattt actacttaaa catagacatg tccaaaatgg gactgatcaa caaggaagag 840
gtcttgctac ctttagacaa tccatatggc aggattactg gtacagtcaa gaggaagctg 900
acttcaaggc tgtga 915

<210> 13

<211> 915

<212> DNA

<213> BABOON

<400> 13

atggccgact accataacaa ctataaaaaag aatgatgaat tggagttgtt ccgaactggc 60
tatgggaagg atatggtaaa agttctccat attcagcgag atggaaaata tcacagcatt 120
aaagaggtgg caacttcagt gcaacttact ctgagttcca aaaaagatta cctgcattgga 180
gataatttcag atatcatccc tacagacacc atcaagaaca cagttcatgt cttggcggaaag 240
tttaaggaa tcaaaaagcat agaaggcttt ggtgtgaata ttttgagta ttttcttct 300
tcttttaacc atgtaatccg agctcaagtc tacgtgaaag aaatcccttg gaagcgtctt 360
gaaaagaatg gagttaaagca tgtccatgca ttatttcaca ctccttactgg aacacacttc 420
tgtgaagttt aacaaactgag aagtggaccc cccgtcattt attctggaaat caaagacctc 480
aaggcttga aaacaacaca gtctggattt gaaggttca tcaaggacca gttcaccacc 540
ctccctgagg tgaaggaccc atgcttgc acccaagtgt actgcaagtg gcgctaccac 600
cagtgcaggg atgtggactt cgaggctacc tggggcacca ttccggaccc tgcctggag 660
aaatttgctg ggccctatga caaaggcgag tactcacccctt ctgtcagaa gaccctctat 720
gatatccagg tgctccctt gagccgagtt cctgagatag aagatatggaa aatcagcctg 780

ccaaacattc actacttcaa tatagacatg tccaaaatgg gtctgatcaa caaggaagag 840
gtcttgctgc cattagacaa tccatatgga aaaattactg gtacagtcaa gaggaagttg 900
tcttcaagac tgtga 915